

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/806,852

Source: _____

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RAW SEQUENCE LISTING

DATE: 12/03/2004

PATENT APPLICATION: US/10/806,852

TIME: 07:22:53

Input Set : N:\Crf3\RULE60\10806852.raw.txt

Output Set: N:\CRF4\12032004\J806852.raw

SEQUENCE LISTING

```

3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: RUEGER, DAVID C.
6           SAMPATH, KUBER T.
7           OPPERMANN, HERMANN
8           PANG, ROY H.L.
9           COHEN, CHARLES M.
11    (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
12           TREATMENT OF MOTOR NEURON INJURY AND NEUROPATHY
14    (iii) NUMBER OF SEQUENCES: 9
16    (iv) CORRESPONDENCE ADDRESS:
17          (A) ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
18                      THIBEAULT, LLP
19          (B) STREET: 125 HIGH STREET
20          (C) CITY: BOSTON
21          (D) STATE: MA
22          (E) COUNTRY: USA
23          (F) ZIP: 02110
25    (v) COMPUTER READABLE FORM:
26          (A) MEDIUM TYPE: Floppy disk
27          (B) COMPUTER: IBM PC compatible
28          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31    (vi) CURRENT APPLICATION DATA:
C--> 37          (A) APPLICATION NUMBER: US/10/806,852
C--> 38          (B) FILING DATE: 23-Mar-2004
34          (C) CLASSIFICATION: 435
36    (viii) ATTORNEY/AGENT INFORMATION:
39          (A) NAME: MEYERS, THOMAS C.
40          (B) REGISTRATION NUMBER: 36,989
41          (C) REFERENCE/DOCKET NUMBER: CRP-155
43    (ix) TELECOMMUNICATION INFORMATION:
44          (A) TELEPHONE: (617) 248-7013
45          (B) TELEFAX: (617) 248-7100
48 (2) INFORMATION FOR SEQ ID NO: 1:
50    (i) SEQUENCE CHARACTERISTICS:
51          (A) LENGTH: 1822 base pairs
52          (B) TYPE: nucleic acid
53          (C) STRANDEDNESS: single
54          (D) TOPOLOGY: linear
56    (ii) MOLECULE TYPE: cDNA
58    (vi) ORIGINAL SOURCE:
59          (A) ORGANISM: HOMO SAPIENS

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60      (F) TISSUE TYPE: HIPPOCAMPUS
62      (ix) FEATURE:
63          (A) NAME/KEY: CDS
64          (B) LOCATION: 49..1341
65          (C) IDENTIFICATION METHOD: experimental
66          (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
67 /product= "OP1"
68 /evidence= EXPERIMENTAL
69 /standard_name= "OP1"
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
75                                         Met His Val
76                                         1
78 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
79 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
80      5      10      15
82 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
83 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
84 20      25      30      35
86 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201
87 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
88      40      45      50
90 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC      249
91 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
92      55      60      65
94 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG      297
95 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
96      70      75      80
98 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC      345
99 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
100      85      90      95
102 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC      393
103 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
104 100      105      110      115
106 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC      441
107 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
108      120      125      130
110 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC      489
111 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
112      135      140      145
114 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC      537
115 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
116      150      155      160
118 CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC      585
119 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
120      165      170      175
122 TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT      633
123 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
124 180      185      190      195

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Input Set : N:\Crif3\RULE60\10806852.raw.txt

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126	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC	681
127	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
128	200 205 210	
130	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC	729
131	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
132	215 220 225	
134	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG	777
135	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
136	230 235 240	
138	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC	825
139	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
140	245 250 255	
142	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC	873
143	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
144	260 265 270 275	
146	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC	921
147	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
148	280 285 290	
150	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC	969
151	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
152	295 300 305	
154	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC	1017
155	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
156	310 315 320	
158	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	1065
159	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
160	325 330 335	
162	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC	1113
163	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
164	340 345 350 355	
166	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG	1161
167	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
168	360 365 370	
170	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC	1209
171	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
172	375 380 385	
174	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC	1257
175	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	
176	390 395 400	
178	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA	1305
179	Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys	
180	405 410 415	
182	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC	1351
183	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
184	420 425 430	
186	GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
188	GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
190	TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC	1531
192	ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC	1591

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194 GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651
196 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711
198 GCGGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771
200 CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822
203 (2) INFORMATION FOR SEQ ID NO: 2:
205     (i) SEQUENCE CHARACTERISTICS:
206         (A) LENGTH: 431 amino acids
207         (B) TYPE: amino acid
208         (D) TOPOLOGY: linear
210     (ii) MOLECULE TYPE: protein
212     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
214 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
215   1           5           10           15
217 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
218           20           25           30
220 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
221           35           40           45
223 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
224           50           55           60
226 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
227   65           70           75           80
229 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
230           85           90           95
232 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
233           100          105          110
235 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
236           115          120          125
238 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
239           130          135          140
241 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
242 145          150          155          160
244 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
245           165          170          175
247 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
248           180          185          190
250 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
251           195          200          205
253 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
254           210          215          220
256 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
257 225          230          235          240
259 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
260           245          250          255
262 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
263           260          265          270
265 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
266           275          280          285
268 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
269           290          295          300

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271 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
272 305                      310                      315                      320
274 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
275                      325                      330                      335
277 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
278                      340                      345                      350
280 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
281                      355                      360                      365
283 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
284                      370                      375                      380
286 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
287 385                      390                      395                      400
289 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
290                      405                      410                      415
292 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
293                      420                      425                      430

```

295 (2) INFORMATION FOR SEQ ID NO: 3:

297 (i) SEQUENCE CHARACTERISTICS:

298 (A) LENGTH: 102 amino acids

299 (B) TYPE: amino acid

300 (C) STRANDEDNESS:

301 (D) TOPOLOGY: linear

303 (ii) MOLECULE TYPE: protein

306 (ix) FEATURE:

307 (A) NAME/KEY: Protein

308 (B) LOCATION: 1..102

309 (D) OTHER INFORMATION: /label= OPX

310 /note= "wherein each Xaa is independently selected from a group

311 of one or more specified amino acids as defined in the

312 specification."

315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

W--> 317 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
318 1 5 10 15
320 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
321 20 25 30
323 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
324 35 40 45
326 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
327 50 55 60
329 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
330 65 70 75 80
332 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
333 85 90 95
335 Xaa Ala Cys Gly Cys His
336 100

```

338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 97 amino acids

342 (B) TYPE: amino acid

RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\Crf3\RULE60\10806852.raw.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos.2,3,9,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
Seq#:3; Xaa Pos.75,80,82,84,87,89,91,97
Seq#:4; Xaa Pos.2,3,4,6,7,8,11,12,13,14,15,16,18,19,20,21,23,26,28,30,31,33
Seq#:4; Xaa Pos.34,35,36,37,38,39,40,44,45,46,47,48,49,50,51,52,53,54,55,56
Seq#:4; Xaa Pos.57,58,59,60,63,65,66,67,68,69,70,71,72,74,75,76,77,78,79,80
Seq#:4; Xaa Pos.82,84,85,86,87,88,90,92,93,95,97
Seq#:5; Xaa Pos.2,3,4,5,7,8,9,11,12,13,16,17,18,19,20,21,23,24,25,26,28,31
Seq#:5; Xaa Pos.33,35,36,38,39,40,41,42,43,44,45,49,50,51,52,53,54,55,56,57
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Seq#:6; Xaa Pos.1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24
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Seq#:6; Xaa Pos.91,92,93,95,97
Seq#:7; Xaa Pos.2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,23,24
Seq#:7; Xaa Pos.25,26,27,28,29,31,33,35,36,37,38,39,40,41,42,43,44,45,46,47
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Seq#:7; Xaa Pos.91,92,93,94,95,96,97,98,100,102
Seq#:8; Xaa Pos.2,3,4,5
Seq#:9; Xaa Pos.2,3,4,5

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10806852.raw.txt

Output Set: N:\CRF4\12032004\J806852.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vi)
L:38 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:341 Repeated in SeqNo=6
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
M:341 Repeated in SeqNo=7
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0